

entor: William Soo Hoo Scket #: P-IM 2442

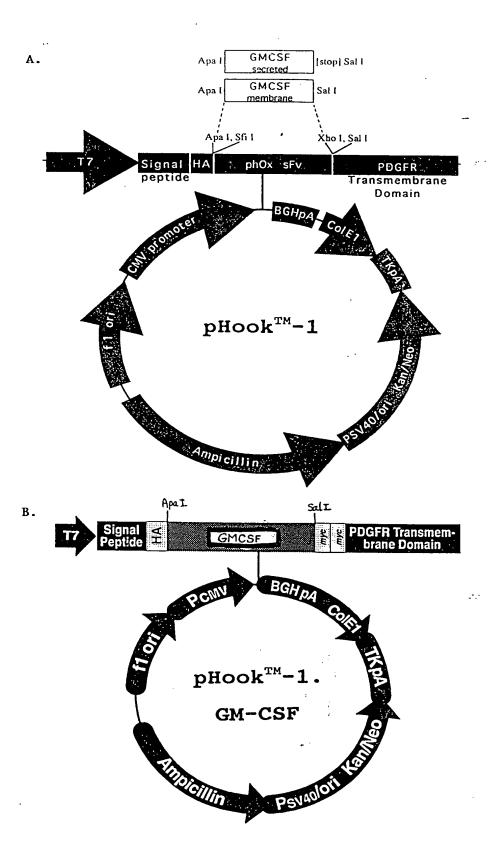


Figure 1

	GTG V	GGA'	A CGC	⊅ ACC	TG2E	<b>&gt;</b>	ATC
tra	GTGCTCACCA TCATCTCCT TATCATCCTC ATCATGCTTT GGCAGAAGAA V L T I I S L I I L I M L W Q K K	r TCTG	410 * * CGGATTTCAT A D F I	310 320 330 ACCAAACTCA AGGGCGCCTT GAACATGACA T K L K G A L N M T	E POR	+ñ	10 20 30  * 10 * 20 * 30  * ATT D T L L W V.
: XSM	T I	510 ;AAT G	410 CAT A	310 TCA A	210 210 V	110 CCG C	10 CAG AC
· A	CATCT	÷ SCTGTG	GACAGO	GGGCC	ENCSF  CARACTC  FA GAAGTC	TCACC	CACAC
۲۶۶	T S T.	520 igacc	420 CCTT	320 CCTT A L	220 GTCT	120 CATC	TCCT L L
م م	TATC	AGGAC Q D	X XAAA	GAAC N	CTAAC		T GCTJ
transmembrane domain	ATCATCCTC	t Si	420 430 440 AGACAGCCTT AAAAACCTTTC TGACTGATAT D S L K T F L T D I	ATGAC	230 CGAGTT	-murine kappa light chain 120 130 130 reacceate actigicacce giccit s p I T V T R P	YIGGG
2	CTC ATC	530 GCA GG	430 TTC TG	330 ACA GC		130 CC 66	
	CATGCT	* BAGGTC E V	ACTG	S CAGC	240 * CTCCTTCAAG S F K	P I	T GCIG
	CTTT	540 CATC	440 ATAT D I	340 FACT Y		140 1GGAA GCA W K H	40 CTCT
	GGCAC	GIGGI	2000	ACCAC Y Q	AAGC	GCAT(	W V
	GGCAGAAGAA W Q K K	550 FIGGIGCCAC V V P	CCCCTITGAA TGCAAAAAAC CAGGCCAAAAA PFECKKPGQK PFECKKPGQK	TACA 3	AAGCTAACAT GTGTGCAGAC	Rappa 134 Chair Signal Squerice 160 170 130 140 150 160 170 ACTGTCACCC GGCCTTGGAA GCATGTAGAG GCCATCAAAG AAGCCCTGAA T V T R P W K H V E A I K E A L N	40 50 60 70 80 90 100  CTGCTGCTCT GGGTTCCAGG TTCCACTGGT GACTATCCAT ATGATGTTCC AGATTATGCT GGGGCCCAAG  L L W V P G S T G D Y P Y D V P D Y A G A Q
	A GCC	O HCI	A TGC	TA CTGC	C GIG	9 GCC	o ricc
د	≈ cci	T S T	TGCAAAAAAC C C K K F C K K F C K K F	d 00000	PIGCAG	ATCA	CACT
		17 P T T T T T T T T T T T T T T T T T T	AAAC CU K P	360 CCA A	260 GAC C	160 AAAG AJ	ရင်ရှိ ရင်ရှိ
	GCGGCCGCTC GAGATCAGCC TCG	CTTTAAGGTG F K V 670	AGGCC	TP	270 * ccgccTGAAG R L K	AGCC(	ACTAI
	A P	AAGGTG	470 CAAAA Q K	370 3GAAA E	270 TGAAG	170 TGAA	70 * TCCAT
	GAGJ R I	v Gra		1 000		CCIO	ATG
	ATCAG	GIGGIGAICT V V I PDGFR	GAC *	ACTGT	TTCGAC	180  CCTCCTGGAT  L L D	ATGTT
	. 20 4 + 20 4	20 20 20 CO 10 10 10 10 10 10 10 10 10 10 10 10 10	_	380 TGA A	280 AGC AC		8 y d
	CGACT R L	AGCCA	AAAAA Q K	T CACA	G G C	ACATG	ATTAT D Y
	r c	CCATCCT A I L A I L 690	490 * * NAACTCA K L	390 CAAGTT Q V	290 TACG	190 CCTG	A 130CT 90
	ACTGTGC CTTCTAG	CAGCCATCCT GGCCCTGGTG S A I L A L V B transmembrane don 690	A490 500  AAACTCA TCTCAGAAGA  K L I S E E  K L I S E 600	370 380 390 400  ACTCCGGAAA CGGACTGTGA AACACAAGTT ACCACCTATG T P E T D C E T Q V T T Y	280 290 300 ATATTCGAGC AGGGTCTACG GGGCAATTTC I F E Q G L R G N F	190 200  GACATGCCTG TCACGTTGAA  D M P V T L N	GGGG
	TAG	CIGGI	* 500 AGAAGA E E E	ACCTATG	AATTIC N F	200 GTTGAA L N	· 100 icccaag
		ccarccr ggcccrggrg  A I L A L V  Raysmembrane domain 690	Ö 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	)   a + c	)   `ñ •ō	N 4 60	ິດ <b>•</b> ວັ
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Figure 2

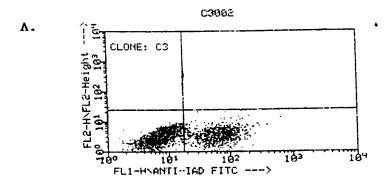
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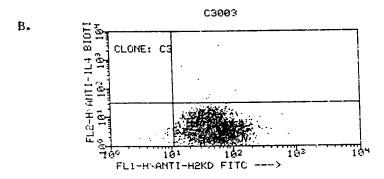
Figure 3

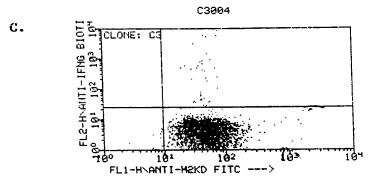


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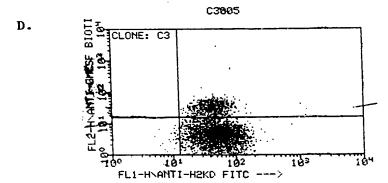


Figure 4